**AMENDMENTS TO SPECIFICATION**

Please replace the title with:

~~CRYSTALLIZABLE JNK COMPLEXES~~ METHODS OF DESIGNING INHIBITORS FOR JNK KINASES

Please replace the paragraph beginning on page 43, line 17, which starts with "Figures 1a-5" with:

Figures [[1a-5,]] 2A, 2B, 3, 4A, 4B and 5 further depict the structure of the JNK3/MgAMP-PNP complex. [[Thus,]] Fig. 1B depicts the structure-based sequence alignment of JNK3 [S. Gupta et al., (1996)], ERK2 [T.G. Boulton et al., Cell, 65, pp. 663-75 (1991)], p38 (J.C. Lee et al., Nature, 372, pp. 739-46 (1994)] and cAPK (M.D. Uhler, Proc. Natl. Acad. Sci. USA, 83, pp. 1300-04 (1986)]. The amino acid sequences of JNK3, human ERK2, human p38 kinase, and murine cAPK are aligned based on structural similarity. The divergent N- and C-terminal regions of Erk2, p38, cAPK are not shown in Fig. 1B. N- and C-terminal residues that are not included in the truncated JNK3 (JNK3: residues Ser40-Glu402) for crystallographic studies are denoted by lowercase letters in Fig. 1B. Residues in italics are not included in the model. Subdomains in Fig. 1B are labeled by Roman numerals

according to S.K. Hanks et al., Science, 241, pp. 42-52 (1988). The secondary structural elements for JNK3 are indicated above the sequences (nomenclature as for Fig. 2A[[a]]), with open boxes designating $\alpha\alpha$ helices and 3/10 helices and open arrows for $\beta\beta$ strands. Disordered regions are indicated with dashed lines. Both JNK3 and cAPK sequence numbering are shown. Phosphorylation sites in the phosphorylation lip are denoted by an asterisk. JNK3 residues that differ from JNK1 and JNK2 are highlighted in bold.